Package 'hutan'

June 3, 2015

Title A Collection of Tools for Phylogenetic Tree Manipulation

Version 0.0.0.9000

Description A collection of tools for phylogenetic tree manipulation. It is named after the Indonesian word for forest.

Depends R (>= 3.1.0)

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LazyData true

Collate 'utility_functions.R'
　　'hutan.R'
　　'siphonophore_constraint.R'
　　'siphonophore_ml.R'

Imports ape (>= 3.3)

Suggests testthat,
　　roxygen2,
　　devtools

R topics documented:

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are_bipartitions_compatible

> *Check if two bipartitions drawn from trees with the same tips are compatible with eachother. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.*

Description

Check if two bipartitions drawn from trees with the same tips are compatible with eachother. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.

Usage

```
are_bipartitions_compatible(bi1, bi2, phy)
```

Arguments

bi1	The first bipartition.
bi2	The second bipartition.
phy	A phylo object describing a tree that includes all tips under investigation. This is used to infer the other half of each bipartition.

Value

TRUE if bi1 is compatible with bi2, otherwise FALSE.

---

bipartition_for_edge   *Get a bipartition, described as a vector of tip numbers, from a specified tree and edge number.*

Description

Get a bipartition, described as a vector of tip numbers, from a specified tree and edge number.

Usage

```
bipartition_for_edge(phy, edge)
```

Arguments

phy	A phylo object that specifies the tree.
edge	The number of the edge that defines the bipartition.

Value

A vector of tip nodes (specified by numbers) that define one half of the bipartition (the other half is the set of tip nodes that are not in this vector).

bipartition_for_edge_by_label

Get a bipartition, described as a vector of tip labels, from a specified tree and edge number.

Description

Get a bipartition, described as a vector of tip labels, from a specified tree and edge number.

Usage

```
bipartition_for_edge_by_label(edge, phy)
```

Arguments

edge	The number of the edge that defines the bipartition.
phy	A phylo object that specifies the tree.

Value

A vector of tip nodes (specified by labels) that define one half of the bipartition (the other half is the set of tip nodes that are not in this vector).

compatible_edges

Identify the edges in one phylo object that are compatible with the edges in another phylo object. Requires the same tip labels for each tree.

Description

Identify the edges in one phylo object that are compatible with the edges in another phylo object. Requires the same tip labels for each tree.

Usage

```
compatible_edges(phy1, phy2)
```

Arguments

phy1	The tree under consideration
phy2	The tree to be compared to

Value

A boolean vector corresponding to the edges in phy1. Each element is FALSE if the edge is iscompatible with phy2, or TRUE if compatible.

| descendants | *Get all the descendants of a given node in a tree.* |

Description

Get all the descendants of a given node in a tree.

Usage

```
descendants(phy, a, keep_node = FALSE)
```

Arguments

phy	A phylo object that specifies the tree.
a	The number of a node in phy.
keep_node	If FALSE, do not include a in the result.

Value

A vector of nodes (specified by number) that are descendants of a. Includes internal and tip nodes.

| get_bipartitions | *Get a list of all the bipartitions in a tree.* |

Description

Get a list of all the bipartitions in a tree.

Usage

```
get_bipartitions(phy)
```

Arguments

phy	A phylo object that specifies the tree.

Value

A list of bipartitions for the tree. The order of the list corresponds to the edges in phy$edge. Bipartitions are specified as a vector of the tip labels that make up one half of the bipartition.

| hutan | *hutan: A collection of tools for phylogenetic tree manipulation.* |

Description

The hutan package provides functions for common phylogenetic tree manipulation tasks, and uses these fascilitate some more specialized tasks. It is named after the Indonesian word for forest.

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is_compatible_with_set

> *Check if bipartition bi is compatible with the bipartitions in bi_list. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.*

Description

Check if bipartition bi is compatible with the bipartitions in bi_list. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.

Usage

```
is_compatible_with_set(bi, bi_list, phy)
```

Arguments

bi	The query bipartition.
bi_list	A list of the bipartitions to be compared against.
phy	A phylo object describing a tree that includes all tips under investigation. This is used to infer the other half of each bipartition.

Value

TRUE if bi is compatible with all bipartition in bi_list, otherwise FALSE.

---

is_monophyletic

> *Test if a set of tips, specified as a vector of tip labels, forms a monophyletic group in a given tree. The test is unrooted, i.e. the group can span the root.*

Description

Test if a set of tips, specified as a vector of tip labels, forms a monophyletic group in a given tree. The test is unrooted, i.e. the group can span the root.

Usage

```
is_monophyletic(phy, x)
```

Arguments

phy	The tree under consideration
x	A vector of the labels of the tips in question

Value

A boolean, TRUE if the tips form a monophyletic group.

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siphonophore_constraint

Siphonophores constraint phylogeny.

Description

An unresolved phylogeny that constrains the group Agalmatidae sensu stricto + Bargmannia to be monophyletic, corresponding to the published SOWH test

Usage

```
siphonophore_constraint
```

Format

An ape phylo object

Source

<http://dx.doi.org/10.1080/10635150500354837>

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siphonophore_ml   *Siphonophores phylogeny.*

Description

A maximum likelihood phylogeny of siphonophores

Usage

```
siphonophore_ml
```

Format

An ape phylo object

Source

<http://dx.doi.org/10.1080/10635150500354837>

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tips *Get tips and labels of a phylo object.*

Description

Get tips and labels of a phylo object.

Usage

```
tips(phy)
```

Arguments

phy   A phylo object.

Value

A vector of all the tips, annotated with their names

---

tip_descendants *Get all the tips that are descendants of a given node in a tree.*

Description

Get all the tips that are descendants of a given node in a tree.

Usage

```
tip_descendants(phy, a)
```

Arguments

phy   A phylo object that specifies the tree.

a   The number of a node in phy.

Value

A vector of tip nodes (specified by number) that are descendants of a. If a is a tip, it is the sole element of this vector.

zero_constrained	*Generates the "zero-constrained" tree described by Susko 2014 (http://dx.doi.org/10.1093/molbev/msu039)*

Description

Generates the "zero-constrained" tree described by Susko 2014 (http://dx.doi.org/10.1093/molbev/msu039)

Usage

```
zero_constrained(phy_resolved, phy_constraint, epsilon = 1e-06)
```

Arguments

phy_resolved   A fully resolved phylogeny stored as a phylo object, e.g. an ML tree.

phy_constraint A partially resolved constraint tree.

epsilon   The value to replace the branch length with

Value

A phylo object containing a tree that is the same as phy_resolved, except that the length of edges that are incompatible with phy_constraint are replaced with epsilon.

Examples

```
data( siphonophore_ml )
data( siphonophore_constraint )
zc <- zero_constrained( siphonophore_ml, siphonophore_constraint )
```

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